

IAP13 Rec'd PCT/PTO 12 DEC 2005

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SEQUENCE LISTING

<110> The Scripps Research Institute
The Regents of the University of California
Wu, Eugene
Nemerow, Glen R.
Stewart, Phoebe

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ggt ggc atg cgt ata aat aac aac ttg tta att cta gat gtg gat tac Gly Gly Met Arg Ile Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr	260	265	270	816
cca ttt gat gctcaa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro	275	280	285	864
ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly	290	295	300	912
cta tac ctt ttt aat gca tca aac aat act aaa aaa ctg gaa gtt agc Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser	305	310	315	960
ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile	325	330	335	1008
aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro	340	345	350	1056
gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn	355	360	365	1104
gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp	370	375	380	1152
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ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp	405	410	415	1248
aat gac tgc aaa ttt act ttg gtt ctt aca aaa tgt ggg agt caa gta Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val	420	425	430	1296
cta gct act gta gct gct ttg gct gta tct gga gat ctt tca tcc atg Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met	435	440	445	1344
aca ggc acc gtt gca agt gtt agt ata ttc ctt aga ttt gac caa aac Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn	450	455	460	1392
ggg gtt cta atg gag aac tcc tca ctt aaa aaa cat tac tgg aac ttt Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe	465	470	475	1440
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 Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
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 Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
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 85 90 95
 Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
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 Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
 115 120 125
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 Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
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 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
 180 185 190
 Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser

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Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala		
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Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly		240
245	250	255
Gly Gly Met Arg Ile Asn Asn Asn Leu Ile Leu Asp Val Asp Tyr		
260	265	270
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro		
275	280	285
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly		
290	295	300
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser		
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Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile		320
325	330	335
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro		
340	345	350
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn		
355	360	365
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp		
370	375	380
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr		
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Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp		400
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Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val		
420	425	430
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met		
435	440	445
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn		
450	455	460
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe		
465	470	475
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly		480
485	490	495
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala		
500	505	510
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys		
515	520	525
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu		
530	535	540
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu		
545	550	555
Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe		560
565	570	575
Ser Tyr Ile Ala Gln Glu		
580		

<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber

<220>
<221> CDS
<222> (1)...(1746)
<400> 34

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atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro 1 5 10 15	48
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro 20 25 30	96
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser 35 40 45	144
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 50 55 60	192
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 65 70 75 80	240
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn 85 90 95	288
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100 105 110	336
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 115 120 125	384
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130 135 140	432
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145 150 155 160	480
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 165 170 175	528
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 180 185 190	576
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 195 200 205	624
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210 215 220	672
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr 225 230 235 240	720
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768

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Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala 245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val 260 265 270	816
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln 275 280 285	864
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn 290 295 300	912
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu 305 310 315 320	960
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile 325 330 335	1008
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro 340 345 350	1056
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp 355 360 365	1104
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp 370 375 380	1152
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr 385 390 395 400	1200
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu 405 410 415	1248
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile 420 425 430	1296
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile 435 440 445	1344
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn 450 455 460	1392
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe 465 470 475 480	1440
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly	1488

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485	490	495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala 500 505 510			1536
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys 515 520 525			1584
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp 530 535 540			1632
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly 545 550 555 560			1680
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser 565 570 575			1728
tac att gcc caa gaa taa Tyr Ile Ala Gln Glu * 580			1746

<210> 35
 <211> 581
 <212> PRT
 <213> Adenovirus serotype 5 fiber

<400> 35		
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro 1 5 10 15		
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro 20 25 30		
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser 35 40 45		
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 50 55 60		
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 65 70 75 80		
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn 85 90 95		
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100 105 110		
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 115 120 125		
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130 135 140		
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145 150 155 160		
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 165 170 175		
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 180 185 190		
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 195 200 205		
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210 215 220		

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Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr
225					230					235					240
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala
										245		250			255
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val
										260		265			270
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln	
										275		280			285
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn
										290		295			300
Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu
										305		310			315
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile
										325		330			335
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro
										340		345			350
Asn	Thr	Asn	Pro	Leu	Lys	Thr	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp
										355		360			365
Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp
										370		375			380
Ser	Thr	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys	Leu	Thr
										385		390			400
Leu	Trp	Thr	Thr	Pro	Ala	Pro	Ser	Pro	Asn	Cys	Arg	Leu	Asn	Ala	Glu
										405		410			415
Lys	Asp	Ala	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile
										420		425			430
Leu	Ala	Thr	Val	Ser	Val	Leu	Ala	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile
										435		440			445
Ser	Gly	Thr	Val	Gln	Ser	Ala	His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn
										450		455			460
Gly	Val	Leu	Leu	Asn	Asn	Ser	Phe	Leu	Asp	Pro	Glu	Tyr	Trp	Asn	Phe
										465		470			480
Arg	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly
										485		490			495
Phe	Met	Pro	Asn	Leu	Ser	Ala	Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala
										500		505			510
Lys	Ser	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	Asn	Gly	Asp	Lys	Thr	Lys
										515		520			525
Pro	Val	Thr	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp
										530		535			540
Thr	Thr	Pro	Ser	Ala	Tyr	Ser	Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly
										545		550			560
His	Asn	Tyr	Ile	Asn	Glu	Ile	Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser
										565		570			575
Tyr	Ile	Ala	Gln	Glu											
															580

<210> 36
<211> 1098
<212> DNA
<213> Adenovirus serotype 37 fiber

<220>
<221> CDS
<222> (1)...(1098)

<400> 36
atg tca aag agg ctc cggtgtggaa gat gac ttc aac ccc gtc tac ccc 48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1 5 10 15

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tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe 20 25 30	96
gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu 35 40 45	144
aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys 50 55 60	192
gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro 65 70 75 80	240
aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr 85 90 95	288
gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly 100 105 110	336
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp 115 120 125	384
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu 130 135 140	432
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val 145 150 155 160	480
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala 165 170 175	528
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr 180 185 190	576
tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu 195 200 205	624
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile 210 215 220	672
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa Val Val Ala Gly Lys Tyr His Ile Ile Asn Lys Thr Asn Pro Lys 225 230 235 240	720
ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu 245 250 255	768

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tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
260 265 270	
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
275 280 285	
aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
290 295 300	
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro	
305 310 315 320	
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
325 330 335	
atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe	
340 345 350	
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *	
355 360 365	

<210> 37

<211> 365

<212> PRT

<213> Adenovirus serotype 37 fiber

<400> 37

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	

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195	200	205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile		
210	215	220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys		
225	230	235
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu		
245	250	255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly		
260	265	270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro		
275	280	285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg		
290	295	300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro		
305	310	315
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser		
325	330	335
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe		
340	345	350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu		
355	360	365

<210> 38

<211> 1098

<212> DNA

<213> Adenovirus serotype 19p fiber

<220>

<221> CDS

<222> (1)...(1098)

<400> 38

atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc	48	
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro		
1	5	10
		15

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt	96	
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe		
20	25	30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc	144	
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu		
35	40	45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag	192	
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys		
50	55	60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct	240	
Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro		
65	70	75
		80

aag gct cca ctg caa gtt act act gat aaa aaa ctt gag ctt gca tat	288	
Lys Ala Pro Leu Gln Val Thr Asp Lys Lys Leu Glu Leu Ala Tyr		
85	90	95

gat aat cca ttt gaa tgt agt gct aat aaa ttt agt tta aaa gta gga	336	
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly		
100	105	110

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cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp 115 120 125	384
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu 130 135 140	432
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val 145 150 155 160	480
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala 165 170 175	528
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Pro Asp Thr 180 185 190	576
tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu 195 200 205	624
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile 210 215 220	672
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu 225 230 235 240	720
ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu 245 250 255	768
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly 260 265 270	816
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro 275 280 285	864
aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg 290 295 300	912
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro 305 310 315 320	960
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser 325 330 335	1008
atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe 340 345 350	1056
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098

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Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*
355												365	

<210> 39
<211> 365
<212> PRT

<213> Adenovirus serotype 19p fiber

<400> 39															
Met	Ser	Lys	Arg	Leu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro
1				5			10				15				
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe
							20		25			30			
Val	Ser	Ser	Asp	Gly	Phe	Lys	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu
						35		40			45				
Lys	Leu	Ala	Asp	Pro	Ile	Thr	Ile	Thr	Asn	Gly	Asp	Val	Ser	Leu	Lys
	50					55				60					
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Ser	Leu	Thr	Val	Asn	Pro
	65					70			75		80				
Lys	Ala	Pro	Leu	Gln	Val	Thr	Thr	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Tyr
						85			90		95				
Asp	Asn	Pro	Phe	Glu	Cys	Ser	Ala	Asn	Lys	Phe	Ser	Leu	Lys	Val	Gly
						100			105		110				
His	Gly	Leu	Lys	Val	Leu	Asp	Glu	Lys	Ser	Ala	Ala	Gly	Leu	Lys	Asp
						115			120		125				
Leu	Ile	Gly	Lys	Leu	Val	Val	Leu	Thr	Gly	Lys	Gly	Ile	Gly	Thr	Glu
	130					135			140						
Asn	Leu	Glu	Asn	Thr	Asp	Gly	Ser	Ser	Arg	Gly	Ile	Gly	Ile	Asn	Val
	145					150			155		160				
Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly	Tyr	Leu	Val	Ala
						165			170		175				
Trp	Asn	Pro	Lys	Tyr	Asp	Thr	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Thr
						180			185		190				
Ser	Pro	Asn	Cys	Thr	Ile	Ala	Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu
						195			200		205				
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile
						210			215		220				
Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Glu
	225					230			235		240				
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu
						245			250		255				
Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala	Tyr	Trp	Asn	Phe	Arg	Ser	Gly
						260			265		270				
Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro
						275			280		285				
Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser	Asn	Ser	Lys	Lys	Tyr	Ala	Arg
						290			295		300				
Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro
	305					310				315		320			
Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser
						325			330		335				
Ile	Thr	Phe	Asp	Phe	Ser	Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe
						340			345		350				
Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu			
						355			360		365				

<210> 40
<211> 1228

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<212> DNA
 <213> Adenovirus serotype 9 fiber

<220>
 <221> CDS
 <222> (50) ... (1138)

<400> 40	aaggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag 58	
	Met Ser Lys	
	1	
	agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac 106	
	Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr	
	5 10 15	
	gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc 154	
	Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser	
	20 25 30 35	
	gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct 202	
	Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala	
	40 45 50	
	gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg 250	
	Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly	
	55 60 65	
	ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat 298	
	Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp	
	70 75 80	
	cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct 346	
	Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala	
	85 90 95	
	cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc 394	
	Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly	
	100 105 110 115	
	ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat 442	
	Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn	
	120 125 130	
	act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat 490	
	Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp	
	135 140 145	
	aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca 538	
	Asn Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Leu Ser	
	150 155 160	
	ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag 586	
	Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys	
	165 170 175	
	cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat 634	
	Arg Thr Leu Trp Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp	
	180 185 190 195	
	cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt 682	

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Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser			
200	205	210	
caa ata ttg gct aat gtg tca tta att gtc gta gat ggt aag tac aaa		730	
Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly Lys Tyr Lys			
215	220	225	
att atc aat aac aat act caa cca gct ctc aaa gga ttt acc att aaa		778	
Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe Thr Ile Lys			
230	235	240	
tta ttg ttt gat gaa aat gga gta ctt atg gaa tct tca aat ctt ggt		826	
Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser Asn Leu Gly			
245	250	255	
aaa tca tat tgg aac ttt aga aat gaa aat tca att atg tca aca gct		874	
Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met Ser Thr Ala			
260	265	270	275
tat gaa aaa gct att gga ttc atg cct aat ttg gta gcc tat cca aaa		922	
Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys			
280	285	290	
cct acc gct ggc tct aaa aaa tat gca aga gat ata gtt tat gga aac		970	
Pro Thr Ala Gly Ser Lys Tyr Ala Arg Asp Ile Val Tyr Gly Asn			
295	300	305	
atc tac ctt ggt gga aag cca gat caa cca gta acc att aaa act acc		1018	
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile Lys Thr Thr			
310	315	320	
ttt aat cag gaa act gga tgt gaa tat tct atc aca ttt gat ttt agt		1066	
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp Phe Ser			
325	330	335	
tgg gcc aag act tat gta aat gtt gaa ttt gaa aca acc tct ttt acc		1114	
Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser Phe Thr			
340	345	350	355
ttt tcc tat atc gcc caa gaa tga aagaccaata aacgtgttt tcatttcaaa	1168		
Phe Ser Tyr Ile Ala Gln Glu *			
360			
attttcatgt atctttattt atttttacac cagcacgggt agtcagtctc ccaccaccag	1228		

<210> 41
<211> 362
<212> PRT
<213> Adenovirus serotype 9 fiber

<400> 41
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1 5 10 15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
20 25 30
Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu
35 40 45
Lys Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys
50 55 60
Val Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val

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65	70	75	80
Asn	Ala	Asp	Pro
		Pro	Leu
		Gln	Leu
			Thr
		Asn	Asn
		Lys	Leu
		Gly	Ile
			Ala
		85	95
Leu	Asp	Ala	Pro
		Phe	Asp
		Val	Ile
		Asp	Asn
		Lys	Leu
			Thr
		Leu	Leu
		100	110
Gly	His	Gly	Leu
		Ser	Ile
		Ile	Thr
		Lys	Glu
			Thr
		115	125
Leu	Arg	Asn	Thr
		Leu	Val
		Val	Leu
			Thr
		Gly	Gly
			Thr
		130	140
Ser	Thr	Asp	Asn
		Gly	Gly
			Thr
		Val	Cys
			Val
		145	155
Gly	Leu	Ser	Phe
		Asn	Asn
		Asp	Gly
			Asp
		Leu	Val
			Ala
		165	175
Glu	Asp	Lys	Arg
		Thr	Thr
		Leu	Trp
			Thr
		Pro	Asp
			Thr
		180	190
Lys	Ile	Asp	Gln
		Asp	Asp
			Ser
		Lys	Lys
			Leu
		195	205
Cys	Gly	Ser	Gln
		Ile	Leu
		Ala	Asn
			Val
		Leu	Ser
			Ile
		210	220
Lys	Tyr	Lys	Ile
		Ile	Asn
			Asn
		Thr	Gln
			Pro
		225	240
Thr	Ile	Lys	Leu
		Leu	Phe
			Asp
			Glu
		245	255
Asn	Leu	Gly	Lys
		Ser	Tyr
		Trp	Asn
			Phe
		Asn	Arg
			Asn
		260	270
Ser	Thr	Ala	Tyr
		Glu	Lys
		Ala	Ile
			Gly
		275	285
Tyr	Pro	Lys	Pro
		Pro	Thr
		Ala	Gly
			Ser
		290	300
Tyr	Gly	Asn	Ile
		Tyr	Leu
			Gly
		295	320
305	310	315	320
Lys	Thr	Thr	Phe
		Phe	Asn
			Gln
		325	335
Asp	Phe	Ser	Trp
			Ala
			Lys
			Thr
		340	350
Ser	Phe	Thr	Phe
			Ser
			Tyr
		355	360

<210> 42
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 third repeat

<400> 42
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys
1 5 10 15
Lys Thr Lys Ser
20

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<210> 43
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5      third repeat
```

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<400> 43
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
1 5 10 15
Lys Thr Lys Ser
20

<210> 44
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat motif

<221> VARIANT
<222> 4
<223> Xaa = Thr or Ser

<400> 44
Thr Thr Val Xaa
1

<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat Consensus Sequence

<221> VARIANT
<222> 3,5,7,13
<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT
<222> 1, 2, 4, 6, 8, 9, 11, 12, 14, 15
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 10
<223> Xaa = Pro or Gly

<400> 45
Xaa
1 5 10 15

<210> 46
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 21st repeat

<400> 46
Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
1 5 10 15

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<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1 5 10 15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa
1 5

<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5D₈ fiber

<221> CDS
<222> (13) ... (1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A,T,C or G

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aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro	771
240 245 250	
gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr	819
255 260 265	
aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser	867
270 275 280 285	
cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn	915
290 295 300	
gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr	963
305 310 315	
cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser	1011
320 325 330	
tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser	1059
335 340 345	
tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa 1112 Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu *	
350 355	
gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca	1164
<210> 51	
<211> 359	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Ad5deltas	
<400> 51	
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys	
85 90 95	
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr	
100 105 110	
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn	
115 120 125	
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu	
130 135 140	

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Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
 145 150 155 160
 Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
 165 170 175
 Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
 180 185 190
 Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
 195 200 205
 Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
 210 215 220
 Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
 225 230 235 240
 Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
 245 250 255
 Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
 260 265 270
 Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
 275 280 285
 Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys
 290 295 300
 Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
 305 310 315 320
 Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
 325 330 335
 Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
 340 345 350
 Phe Ser Tyr Ile Ala Gln Glu
 355

<210> 52
<211> 1920
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37k fiber

<221> CDS
<222> (13) ... (1755)

<221> misc_feature
<222> 1867, 1875
<223> n = A,T,C or G

<400> 52

gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30 35 40 45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
 50 55 60

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ctt	gcf	ctc	aaa	atg	ggc	aac	ggc	ctc	tct	ctg	gac	gag	gcc	ggc	aac	243
Leu	Ala	Leu	Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	
65								70					75			
ctt	acc	tcc	caa	aat	gtt	acc	act	gtg	agc	cca	cct	ctc	aaa	aaa	acc	291
Leu	Thr	Ser	Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	
80								85					90			
aag	tca	aac	ata	aac	ctg	gaa	ata	tct	gca	ccc	ctc	aca	gtt	acc	tca	339
Lys	Ser	Asn	Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	
95								100					105			
gaa	gcc	cta	act	gtg	gct	gcc	gcc	gca	cct	cta	atg	gtc	gcg	ggc	aac	387
Glu	Ala	Leu	Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	
110								115					120			125
aca	ctc	acc	atg	caa	tca	cag	gcc	ccg	cta	acc	gtg	cac	gac	tcc	aaa	435
Thr	Leu	Thr	Met	Gln	Ser	Gln	Ala	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys
130								135					140			
ctt	agc	att	gcc	acc	caa	gga	ccc	cct	aca	gtg	tca	gaa	gga	aag	cta	483
Leu	Ser	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	
145								150					155			
gcc	ctg	caa	aca	tca	ggc	ccc	ctc	acc	acc	acc	acc	gat	agc	agt	acc	531
Ala	Leu	Gln	Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Ser	Thr	Leu
160								165					170			
act	atc	act	gcc	tca	ccc	cct	cta	act	act	gcc	act	ggt	agc	ttg	ggc	579
Thr	Ile	Thr	Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	
175								180					185			
att	gac	ttg	aaa	gag	ccc	att	tat	aca	caa	aat	gga	aaa	cta	gga	cta	627
Ile	Asp	Leu	Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	
190								195					200			205
aag	tac	ggg	gct	cct	ttg	cat	gta	aca	gac	gac	cta	aac	act	ttg	acc	675
Lys	Tyr	Gly	Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	
210								215					220			
gta	gca	act	ggg	cca	ggg	gtg	act	att	aat	aat	act	tcc	ttg	caa	act	723
Val	Ala	Thr	Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	
225								230					235			
aaa	gtt	act	gga	gcc	ttg	ggg	ttt	gat	tca	caa	ggc	aat	atg	caa	ctt	771
Lys	Val	Thr	Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	
240								245					250			
aat	gta	gca	gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	819
Asn	Val	Ala	Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	
255								260					265			
ctt	gat	gtt	agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	867
Leu	Asp	Val	Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Gln	Leu	Asn	Leu	Arg		
270								275					280			285
cta	gga	cag	ggc	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	915
Leu	Gly	Gln	Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	
290								295					300			

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aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys 305 310 315	963
aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala 320 325 330	1011
aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro 335 340 345	1059
aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu 350 355 360 365	1107
gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu 370 375 380	1155
agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp 385 390 395	1203
aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att Lys Leu Thr Leu Trp Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile 400 405 410	1251
gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly 415 420 425	1299
agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr 430 435 440 445	1347
cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile 450 455 460	1395
aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu 465 470 475	1443
gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr 480 485 490	1491
gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro 495 500 505	1539
aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr 510 515 520 525	1587
ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr 530 535 540	1635
ttt aaccaa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt	1683

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Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser		
545	550	555
tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc	1731	
Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr		
560	565	570
ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg	1785	
Phe Ser Tyr Ile Ala Gln Glu *		
575	580	
tttaaacccg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgttgcc	1845	
cctccccctg gccttccttg ancctggaa gtgcactcc cactgtcctt tcctaataaa	1905	
atgaggaat gcata		1920
<210> 53		
<211> 580		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Ad5s/Ad37k		
<400> 53		
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro		
1 5 10 15		
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro		
20 25 30		
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser		
35 40 45		
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu		
50 55 60		
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser		
65 70 75 80		
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn		
85 90 95		
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu		
100 105 110		
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr		
115 120 125		
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile		
130 135 140		
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln		
145 150 155 160		
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr		
165 170 175		
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu		
180 185 190		
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly		
195 200 205		
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr		
210 215 220		
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr		
225 230 235 240		
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala		
245 250 255		
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val		
260 265 270		
Ser Tyr Pro Phe Asp Ala Gln Asn Leu Asn Leu Arg Leu Gly Gln		
275 280 285		
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn		

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290	295	300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu		
305	310	315
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile		320
325	330	335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro		
340	345	350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp		
355	360	365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp		
370	375	380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr		
385	390	395
Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp		400
405	410	415
Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile		
420	425	430
Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile		
435	440	445
Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu		
450	455	460
Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala		
465	470	475
Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu		
485	490	495
Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser		
500	505	510
Asn Ser Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu		
515	520	525
Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln		
530	535	540
Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys		
545	550	555
Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr		
565	570	575
Ile Ala Gln Glu		
580		

<210> 54
<211> 1767
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s fiber

<221> CDS
<222> (13) ... (1749)

<400> 54
atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly

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30	35	40	45	
gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met 50	55	60		195
ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser 65	70	75		243
cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn 80	85	90		291
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 95	100	105		339
act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 110	115	120	125	387
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130	135	140		435
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145	150	155		483
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 160	165	170		531
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 175	180	185		579
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 190	195	200	205	627
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210	215	220		675
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr 225	230	235		723
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala 240	245	250		771
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val 255	260	265		819
agt tat ccg ttt gat gct caa aac caa aat cta aga cta gga cag Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln 270	275	280	285	867

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ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn 290 295 300	915
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu 305 310 315	963
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile 320 325 330	1011
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro 335 340 345	1059
aac aca aat ccc ctc aaa aca aaaa att ggc cat ggc cta gaa ttt gat Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp 350 355 360 365	1107
tca aac att ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac Ser Asn Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp 370 375 380	1155
aat gat ggt gcc att aca gta gga aac aaa aat aat gat aag cta act Asn Asp Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr 385 390 395	1203
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu 400 405 410	1251
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile 415 420 425	1299
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile 430 435 440 445	1347
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn 450 455 460	1395
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe 465 470 475	1443
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly 480 485 490	1491
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala 495 500 505	1539
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys 510 515 520 525	1587

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cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac	1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	
530 535 540	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc	1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly	
545 550 555	
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca	1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser	
560 565 570	
tac att gcc caa gaa taa agaagcggcc gcgttatg	1767
Tyr Ile Ala Gln Glu *	
575	

<210> 55
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s

<400> 55	
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val	
65 70 75 80	
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu	
85 90 95	
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala	
100 105 110	
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser	
115 120 125	
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln	
130 135 140	
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Gln Thr Ser Gly	
145 150 155 160	
Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro	
165 170 175	
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro	
180 185 190	
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu	
195 200 205	
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly	
210 215 220	
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu	
225 230 235 240	
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu	
245 250 255	
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro	
260 265 270	
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu	

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275	280	285
Phe Ile Asn Ser Ala His Asn	Leu Asp Ile Asn	Tyr Asn Lys Gly Leu
290	295	300
Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys	Lys Leu Glu Val Asn	Leu
305	310	315
Ser Thr Ala Lys Gly Leu Met Phe Asp	Ala Thr Ala Ile Ala	Ile Asn
325	330	335
Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn	Ala Pro Asn Thr Asn	
340	345	350
Pro Leu Lys Thr Lys Ile Gly His	Gly Leu Glu Phe Asp Ser Asn	Ile
355	360	365
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu	Thr Phe Asp Asn Asp	Gly
370	375	380
Ala Ile Thr Val Gly Asn Lys Asn Asn Asp	Lys Leu Thr Leu Trp	Trp Thr
385	390	395
Thr Pro Ala Pro Ser Pro Asn Cys Arg	Leu Asn Ala Glu Lys Asp	Ala
405	410	415
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln	Ile Leu Ala Thr	
420	425	430
Val Ser Val Leu Ala Val Lys Gly Ser	Leu Ala Pro Ile Ser Gly	Thr
435	440	445
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp	Glu Asn Gly Val	Leu
450	455	460
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr	Trp Asn Phe Arg Asn	Gly
465	470	475
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn	Ala Val Gly Phe Met	Pro
485	490	495
Asn Leu Ser Ala Tyr Pro Lys Ser His	Gly Lys Thr Ala Lys Ser	Asn
500	505	510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp	Lys Thr Lys Pro Val	Thr
515	520	525
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu	Thr Gly Asp Thr Thr	Pro
530	535	540
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp	Trp Ser Gly His Asn	Tyr
545	550	555
Ile Asn Glu Ile Phe Ala Thr Ser Ser	Tyr Thr Phe Ser Tyr	Ile Ala
565	570	575
Gln Glu		

<210> 56
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad37s/Ad5k fiber

<221> CDS
<222> (16)...(1116)

<221> misc_feature
<222> 1125
<223> n = A,T,C or G

<400> 56
gtcgcaagat ccaag atg aag agg gcc cgg ccc agc gaa gat gac ttc aac 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
1 5 10

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ccc gtc tac ccc tat ggc tac gcg cg ^g aat cag aat atc ccc ttc ctc Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu 15 20 25	99
act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly 30 35 40	147
gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp 45 50 55 60	195
gta tcc ctc aag gt ^g gga ggt ggt ctc act ttg caa gat gga agc cta Val Ser Leu Lys Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu 65 70 75	243
act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu 80 85 90	291
gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser 95 100 105	339
tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala 110 115 120	387
ggg tta aaa gat tta att ggc aaa ctt gt ^g gtt tta aca gga aaa gga Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly 125 130 135 140	435
ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile 145 150 155	483
gg ^t ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly 160 165 170	531
tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr 175 180 185	579
aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala 190 195 200	627
aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr 205 210 215 220	675
gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr 225 230 235	723
gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gt ^g cta Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu 240 245 250	771
cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga	819

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Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
 255 260 265
 gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct 867
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
 270 275 280
 sac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac 915
 Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
 285 290 295 300
 att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca 963
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
 305 310 315
 cta acc att aca aac ggt aca cag gaa aca gga gac aca act cca 1011
 Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
 320 325 330
 agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac 1059
 Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
 335 340 345
 att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc 1107
 Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
 350 355 360
 caa gaa taa agaagcggnc gctcga 1132
 Gln Glu *
 365

<210> 57
 <211> 366
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad37s/Ad5k

<400> 57
 Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80
 Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95
 Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
 100 105 110
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160

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Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly	Tyr	Leu	Val	Ala
					165				170						175
Trp	Asn	Pro	Lys	Tyr	Asp	Thr	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Ala	Pro
					180			185					190		
Ser	Pro	Asn	Cys	Arg	Leu	Asn	Ala	Glu	Lys	Asp	Ala	Lys	Leu	Thr	Leu
					195			200				205			
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Thr	Val	Ser	Val	Leu
					210			215			220				
Ala	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile	Ser	Gly	Thr	Val	Gln	Ser	Ala
					225		230		235				240		
His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn	Gly	Val	Leu	Leu	Asn	Asn	Ser
					245			250					255		
Phe	Leu	Asp	Pro	Glu	Tyr	Trp	Asn	Phe	Arg	Asn	Gly	Asp	Leu	Thr	Glu
					260			265				270			
Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly	Phe	Met	Pro	Asn	Leu	Ser	Ala
					275			280				285			
Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala	Lys	Ser	Asn	Ile	Val	Ser	Gln
					290		295				300				
Val	Tyr	Leu	Asn	Gly	Asp	Lys	Thr	Lys	Pro	Val	Thr	Leu	Thr	Ile	Thr
					305		310		315				320		
Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp	Thr	Thr	Pro	Ser	Ala	Tyr	Ser
					325			330				335			
Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly	His	Asn	Tyr	Ile	Asn	Glu	Ile
					340			345				350			
Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu		
					355			360				365			

<210> 58

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad37 third repeat

<400> 58

Gly	Ser	Leu	Thr	Val	Asn	Pro	Lys	Ala	Pro	Leu	Gln	Val	Asn	Thr	Asp
1				5					10				15		

<210> 59

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad8 last repeat

<400> 59

Val	Arg	Val	Gly	Glu	Gly	Gly	Leu	Ser	Phe	Asn	Asp	Asn			
1				5			10								

<210> 60

<211> 14

<212> PRT

<213> Artificial Sequence

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